Listing of Claims:

Please **amend** the claims as follows:

Claim 1 **(Cancelled)**

Claim 2 **(Withdrawn)**

Claim 3 **(Withdrawn)**

Claim 4 **(Withdrawn)**

Claim 5 **(Withdrawn)**

Claim 6 **(Currently Amended)** A method for identifying a virulence gene of *M. tuberculosis*, comprising ~~identifying a virulence gene of *M. marinum* bacterium according to the method of claim 1, and further comprising,~~

a) mutagenizing an *M. marinum* bacterium by introducing into the bacterium a plasmid which comprises a signature-tagged transposon, whereby the transposon integrates into and disrupts a gene in the bacterium,

b) introducing the mutagenized bacterium into a host susceptible to infection thereof,

c) identifying a bacterium which comprises a signature tagged transposon and which exhibits reduced viability in the host, compared to a non-mutagenized *M. marinum* bacterium,

d) cloning and/or sequencing a nucleic acid sequence which flanks the integrated transposon in said identified bacterium, and

e) identifying a wild type *M. marinum* gene which comprises at least a portion of said flanking sequence.

f) comparing said flanking nucleic acid sequence to a databank of *M. tuberculosis* nucleic acid sequences, and/or comparing the sequences of peptides which are coded for by said flanking sequences to a known *M. tuberculosis* protein database, and

g) dentifying an *M. tuberculosis* gene which comprises a sequence that is substantially identical to said flanking sequences.

Claim 7 **(Previously Presented)** A method for generating an avirulent *M. tuberculosis* bacterium, comprising mutagenizing an *M. tuberculosis* virulence gene identified by the method of claim 6.

Claim 8 **(Previously Presented)** An avirulent *M. tuberculosis* bacterium, produced by the method of claim 7.

Claim 9 **(Previously Presented)** An avirulent *M. tuberculosis* bacterium, in which one or more of genes Rv0822c, Rv3137, or Rv2348c, is mutated to render the *M. tuberculosis* bacterium less virulent.

Claim 10 **(Previously Presented)** An avirulent *M. tuberculosis* bacterium of claim 9, in which gene Rv0822c is mutated.

Claim 11 **(Cancelled)**

Claim 12 **(Cancelled)**

Claim 13 **(Cancelled)**

Claim 14 **(Cancelled)**

Claim 15 **(Cancelled)**

Claim 16 **(Cancelled)**

Claim 17 **(Cancelled)**

Claim 18 **(Cancelled)**

Claim 19 **(Cancelled)**

Claim 20 **(Cancelled)**

Claim 21 **(Previously Presented)** An avirulent *M. tuberculosis* bacterium of claim 9, in which gene Rv3137 is mutated.

Claim 22 **(Previously Presented** An avirulent *M. tuberculosis* bacterium of claim 9, in which gene Rv2348c is mutated.

Claim 23 **(Cancelled)**

Claim 24 **(Cancelled)**

Claim 25 **(Previously Presented)** An avirulent *M. tuberculosis* bacterium of claim 9, in which gene Rv2181, Rv1954c, Rv0987, Rv3268, or Rv2610c is mutated.

Claim 26 **(Cancelled)**

Claim 27 **(Cancelled)**

Claim 28 **(Cancelled)**

Claim 29 **(Cancelled)**

Claim 30 **(Cancelled)**

Claim 31 **(Cancelled)**

Claim 32 **(Cancelled)**

Claim 33 **(Cancelled)**

Claim 34 **(Cancelled)**

Claim 35 **(Cancelled)**

Claim 36 **(Cancelled)**

Claim 37 **(Cancelled)**

Claim 38 **(Cancelled)**

Claim 39 **(Cancelled)**

Claim 40 **(Cancelled)**

Claim 41 **(Withdrawn)** A pharmaceutical composition, comprising an avirulent *M. marinum* bacterium of claim 5 and a pharmaceutically acceptable carrier.

Claim 42 **(Withdrawn)** An attenuated *M. marinum* vaccine, comprising an avirulent *M. marinum* bacterium of claim 5 and a pharmaceutically acceptable carrier.

Claim 43 **(Previously Presented)** A pharmaceutical composition, comprising an avirulent *M. tuberculosis* bacterium of claim 9 and a pharmaceutically acceptable carrier.

Claim 44 **(Previously Presented)** An attenuated *M. tuberculosis* vaccine, comprising an avirulent *M. tuberculosis* bacterium of claim 9 and a pharmaceutically acceptable carrier.

Claim 45 **(Previously Presented)** An attenuated *M. tuberculosis* vaccine, comprising an avirulent *M. tuberculosis* bacterium which comprises one or more mutations in one or more virulence genes identified by the method of claim 7 and a pharmaceutically acceptable carrier.

Claim 46 **(Withdrawn)** A method to elicit an immune response in a fish in need of such treatment, comprising administering to said fish an avirulent *M. marinum* bacterium of claim 5.

Claim 47 **(Currently Amended)** A method to elicit an immune response in a patient ~~in need of such treatment~~, comprising administering to said patient an avirulent *M. tuberculosis* bacterium of claim 9.

Claim 48 **(Cancelled)**

Claim 49 **(Cancelled)**

Claim 50 **(Withdrawn)** A method for isolating a mutagenized *M. marinum* bacterium which exhibits reduced virulence in a host susceptible to infection thereof compared to a non-mutagenized *M. marinum* bacterium, comprising integrating a tagged transposon into the DNA of a *M. marinum* bacterium in a manner effective to produced reduced virulence, and isolating said mutagenized bacterium.

Claim 51 **(Cancelled)**

Claim 52 **(Cancelled)**

Claim 53 **(Cancelled)**

Claim 54 **(Cancelled)**

Claim 55 **(Cancelled)**

Claim 56 **(Cancelled)**

Claim 57 **(Cancelled)**

Claim 58 **(Cancelled)**

Claim 59 **(Cancelled)**

Claim 60 **(Cancelled)**

Claim 61 **(Cancelled)**

Claim 62 **(Cancelled)**

Claim 63 **(Cancelled)**

Claim 64 **(Cancelled)**

Claim 65 **(Cancelled)**

Claim 66 **(Cancelled)**

Claim 67 **(Cancelled)**

Claim 68 **(Cancelled)**

Claim 69 **(Cancelled)**

Claim 70 **(Cancelled)**

Claim 71 **(Cancelled)**

Claim 72 **(Cancelled)**

Claim 73 **(Cancelled)**

Claim 74 **(Cancelled)**

Claim 75 **(Cancelled)**

Claim 76 **(Cancelled)**

Claim 77 **(Previously Presented)** An avirulent *M. marinum* bacterium, in which a gene has been disrupted adjacent to a nucleic acid of SEQ ID NOs: 4, 13, 23, 25, or 31.

Claim 78 **(Previously Presented)** An isolated *M. marinum* nucleic acid comprising the oligonucleotide of SEQ ID NOs: 4, 13, 23, 25, or 31, or a fragment or variant thereof; or which is complementary to, or which can hybridize under high stringency conditions to, at least a portion of said isolated nucleic acid or variant thereof.

Claim 79 (Previously Presented) A method to identify an agent which reduces the ability of an *M. tuberculosis* bacterium to survive in a host, comprising

a) overexpressing one of the following *M. tuberculosis* genes: Rv0822c, Rv3137 or Rv2348c in an *M. tuberculosis* bacterium,

b) exposing said bacterium to a putative agent, and

c) determining if the agent reduces the viability or growth of a wild type bacterium, but not the bacterium which overexpresses said gene, in a host.

Claim 80 (Previously Presented) An antibody against a polypeptide encoded by one of the following *M. tuberculosis* genes: Rv0822c, Rv3137 or Rv2348c.

Claim 81 (Previously Presented) An antibody against a peptide encoded by one of the following *M. marinum* polynucleotides: SEQ ID NOs: 4, 13, 23, 25, or 31.

Claim 82 (Previously Presented) An avirulent *M. marinum* bacterium, in which a gene comprising a nucleic acid that is at least 95% identical to SEQ ID NO: 4 is mutated.

Claim 83 (Previously Presented) An avirulent *M. marinum* bacterium of claim 82, wherein the nucleic acid comprises nucleotides 19 to 129 of SEQ ID NO: 4.

Claim 84 (Previously Presented) An avirulent *M. tuberculosis* bacterium, in which a polyketide gene is mutated to render the *M. tuberculosis* bacterium less virulent.

Claim 85 (Previously Presented) An avirulent *M. tuberculosis* bacterium of claim 84, in which the mutated polyketide gene is pks6 (Rv0405).

Claim 86 (Previously Presented) An avirulent *M. tuberculosis* bacterium of claim 84, in which the mutated polyketide gene is pks9 (Rv1664).

Claim 87 (Previously Presented) An avirulent *M. tuberculosis* bacterium of claim 84, in which the mutated polyketide gene is pks8 (Rv1662).

Claim 88 (Previously Presented) An avirulent *M. tuberculosis* bacterium of claim 84, in which the mutated polyketide gene is pks1 (Rv2946c).

Claim 89 (Previously Presented) An avirulent *M. tuberculosis* bacterium of claim 84, wherein said polyketide gene sequence is at least 95% identical to SEQ ID NO: 8.